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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Connective Tissue Growth Factor - 1

Inventors (please provide full names): Li et al Point of Contact: Mona Smith

Earliest Priority Filing Date: 7/8/99 Technical Info. Specialist: CM1 12C14 Tel: 308-3278

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

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USPT,JPAB,EPAB,DWPI,TDBD	(li-haodong.in. or li-h\$.in.) and ctgf	5	<u>L5</u>
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Set	Items	Description
S1	1	CTGF2
S2	1209	CONNECTIVE(W) TISSUE(W) GROWTH(W) FACTOR?
S3	25	S2(S)ISOFORM?
S4	7	RD (unique items)
S5	2	AU=(ADAMS MARK OR ADAMS,M? OR ADAMS M? OR ADAMS, MARK) AND CTGF?
S6	2	RD (unique items)
S7	3	AU=(LI HAODONG OR LI, HAODONG OR LI H? OR LI, H?) AND CTGF
S8	3	RD (unique items)

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OM Protein - protein search, using sw model

Run on: January 8, 2001, 10:36:00 ; Search time 17.32 Seconds

(without alignments)
1493.658 Million cell updates/sec

Title: US-09-348-815-2

Perfect score: 21.15
Sequence: 1 MSSRARALARALAVTLLHLTR... ANEAAPPYRLFNDIHKFRD 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 6790655 residues

Total number of hits satisfying chosen parameters:

195891

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : PIR_66;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8 Result No. Score Query Match Length DB ID

Result No.	Score	Query Match	Length	DB	ID	Description	
1	1938	91.6	379	2	A35669	gene CYR61 protein precursor - mouse	
2	1699	80.3	375	2	A41128	gene CYR61 protein precursor - mouse	
3	952.5	45.2	348	2	A40578	gene CYR61 protein precursor - mouse	
4	951	45.0	348	2	A53228	beta 1G-M2 protein	
5	855.5	45.0	349	2	A40551	beta 1G-M2 protein	
6	7	834.5	40.4	351	2	A50078	fish-12 protein precursor
7	834.5	39.5	357	2	A38069	connective tissue NOV protein - chick	
8	175.5	8.3	1620	2	T27283	gene novH protein	
9	174	8.2	1111	2	T26972	hypothetical protein	
10	159	7.5	1700	2	S08167	Balbiani ring 3 protein	
11	156	7.4	1574	2	T13954	MEG6 protein - rat	
12	153	7.2	837	2	A42112	mucin-like peptide	
13	152.5	7.2	1178	2	A39804	thrombospondin precursor	
14	152	7.2	5376	2	T42215	zonadhesin - mouse	
15	147.5	7.0	1101	2	A53612	laminin B1 chain	
16	145	6.9	601	2	T22025	hypothetical protein	
17	144	6.8	1964	2	T09059	notch4 - mouse	
18	142	6.7	1025	2	T42626	secreted leucine-rich mucin - rat	
19	141.5	6.7	1034	2	JC5595	hypothetical protein	
20	141.5	6.7	1101	2	T16840	mucin, submaxillary mucin 2 precursor	
21	141.5	6.7	13288	2	T03099	notch protein - mouse	
22	141	6.7	3020	2	A43932	5AC (clone L)	
23	140.5	6.6	2703	1	A24420	cysteine-rich protein	
24	139	6.6	1042	2	A57534	transmembrane protein	
25	138	6.5	251	2	A50035	notch protein homo	
26	138	6.5	2437	2	S42612	tenascin-X - bovin	
27	136	6.4	2531	2	S18188	adhesive plaque pr	
28	136	6.4	4135	2	T42629		
29	135	6.4	473	2	A56175		

ALIGNMENTS

30	135	6.4	1168	2	I56985	kalnkin B1 - mouse
31	134	6.3	1056	2	A53767	mucin MDC5B, tracheal fibrillin 1 precursor
32	134	6.3	3002	2	A47221	gene shuttle craft
33	133.5	6.3	1106	2	T13938	slit protein 1 precursor
34	133.5	6.3	1480	2	A36665	agrin precursor - thrombospondin 1 protein
35	133.5	6.3	1955	1	AGCH	hypothetical protein
36	133	6.3	1170	2	A40558	von Willebrand factor
37	133	6.3	1296	2	T16859	laminin alpha-2 chain
38	133	6.3	2813	1	VWHU	hypothetical protein
39	133	6.3	3106	1	S53868	Probable laminin a
40	133	6.3	3672	2	T23438	hypothetical protein
41	133	6.3	3704	2	T31316	Probable laminin a
42	132.5	6.3	1106	2	T44598	hypothetical protein
43	132.5	6.3	1847	2	T18308	Probable vitelline
44	132	6.3	2555	2	A0043	notch protein homo
45	132	6.2	2823	2	T23064	hypothetical protein

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Db 179 -LGLDASEVELTRNNELIAIGKGSLLRKLPLVFGTEPRVLFNPLHAHGQKCTIVQTTSHSQ 236
 Qy 239 CSKTCGIGLISTRYTNDNPECRLVKETRICEVRGQPYSSLKKGKCSKTRKSPEPYRF 298
 Db 237 CSKTCGIGLISTRYTNDNPECRLVKETRICEVRGQPYSSLKKGKCSKTRKSPEPYRF 296
 Qy 299 TYAGCLSVKKYRKPYCSCVDGRCCTPQLTRVTKMFRCEDETFSKNMVMTQSCKCNY 358
 Db 297 TYAGCLSVKKYRKPYCSCVDGRCCTPQLTRVTKMFRCEDETFSKNMVMTQSCKCNY 356
 Qy 359 CPHANEAAFPYRFLNDIHKFRD 381
 Db 357 CPHNEASFRLYSLNDIHKFRD 379

RESULT 2

Qy 1 MSSRARIARALAVYTLHL-TRIAL-STCPAACHCPL-EAPKCAPGVLVDRGCGCKVCA 57
 Db 1 MLASVAGPISLAVLLALCTPATGQDCSACQCAAEAPICPAGYSLVLDGCGCRVA 60
 Qy 58 KOLNEDSKTQPCDHTKGLCNGFASSTALKGICRAQSEGSRPCEYNSTRIYONGESFQPNC 117
 Db 61 KOLGEELCTERPCDPIKGLFDEGSPANRKIGVCTAK-DAAPCYFGSYRSGESFQSSC 119
 Qy 118 KHQCTC1DGAVGCIPLCPOELSLPNIGCPNPRLVKTGQOCEEWVCDDETSIKDPMEDQG 177
 Db 120 KYQCTC1DGAVGCPUCMSMVRPLSPDCPFPVRLPGKCEEWYCDP----- 168
 Qy 178 LIGKELGFDAESEVELTRNNELIAYVGSSKURL -PVFGMPRLYNPLOGKCIYQTTW 236
 Db 169 -----KRTAVGPALAAVRLDFTGPPPTMM ---- RANCLVQTTW 205
 Qy 237 SQCSKTCGTTGISTRTVNDNEPCLVKETRICEVRPGQPYSSLKKGKCSKTRKSPPV 296
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 Qy 357 YNCPHANPAEEPPY -RLFDI 376
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RESULT 4

Qy 120 QCTC1DGAVGCIPLCPOELSLPNIGCPNPRLVKTGQCEEWVCDPESIKDPMEDQGLL 179
 Db 120 QCTC1DGAVGCIPLCPOELSLPNIGCPNPRLVKTGQCEEWVCDES -KDALELEGGF 177
 Qy 180 GRELGFDAESEVELTRNNELIAYVGKGSLLKRLFVGMF - RILYNPLQGQKCIYQTTWS 237
 Db 178 SKEFGDASEGELTRNNELIAYVGKGSLLKRLFVGMF - RILYNPLQGQKCIYQTTWS 232
 Qy 238 QCSKTCGTTGISTRTVNDNEPCLVKETRICEVRGQPYSSLKKGKCSKTRKSPEPYRF 297
 Db 233 QCSKTCGTTGISTRTVNDNEPCLVKETRICEVRGQPYSSLKKGKCSKTRKSPEPYRF 292
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 Qy 58 KOLNEDSKTQPCDHTKGLCNGFASSTALKGICRAQSEGSRPCEYNSTRIYONGESFQPNC 117
 Db 61 KOLGEELCTERPCDPIKGLFDEGSPANRKIGVCTAK-DAAPCYFGSYRSGESFQSSC 119

A;Title: Identification of a gene family regulated by transforming growth factor-beta
 A;Reference number: A40578; MUID:91229699

A;Accession: A40578

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-348
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A;Molecule type: mRNA

A;Residues: 1-348
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A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-375 <SIM>

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A;Molecule type: mRNA

A;Residues: 1-375 <SIM>

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A;Residues: 1-375 <SIM>

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INTERPRO; IPR000867; -.
 DR INTERPRO; IPR000884; -.
 DR INTERPRO; IPR01007; -.
 DR PFAM; PF00007; Cys_knot; 1.
 PFAM; PF00090; tsp_1; 1.
 DR PFAM; PF00093; wvc_1; 1.
 DR PROSITE; PS00222; IGF_BINDING; 1.
 DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS01208; WFPC; 1.
 Growth factor binding: Signal.
 SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 381 CYR61 PROTEIN.
 FT DOMAIN 98 164 WFPC.
 FT DOMAIN 286 360 CTCK.
 DISULFID 286 323 BY SIMILARITY.
 FT DISULFID 303 337 BY SIMILARITY.
 FT DISULFID 314 353 BY SIMILARITY.
 FT DISULFID 317 355 BY SIMILARITY.
 FT DISULFID 322 359 BY SIMILARITY.
 FT CONFLICT 210 210 L -> I (IN REF. 4).
 FT CONFLICT 220 220 L -> R (IN REF. 4).
 SQ SEQUENCE 381 AA; 42026 MW: FC0BD39C078CA0B1 CRC64;
 Query Match Similarity 100.0%; Score 2115; DB 1; Length 381;
 Best Local Similarity 100.0%; Pred. No. 3.9e-154; Gaps 0;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSSRALARALAYVTLHLTRALSTCPAACHCPLAEPKCAPAVGLYRVDGCGCKYCAKQL 60
 Db 1 MSSRALARALAYVTLHLTRALSTCPAACHCPLAEPKCAPAVGLYRVDGCGCKYCAKQL 60
 Qy 61 NEDCSKTPQCDHTKGBCNFASTALKICRAQSGRPCYNSRIVQNGESFOPNCKHQ 120
 Db 61 NEDCSKTPQCDHTKGBCNFASTALKICRAQSGRPCYNSRIVQNGESFOPNCKHQ 120
 Qy 121 CTCIDGAYGCP1PLCPOELSPLNQGPNPRLVYKVTQGCCCEWVCEDESIKDPMDODGLG 180
 Db 121 CTCIDGAYGCP1PLCPOELSPLNQGPNPRLVYKVTQGCCCEWVCEDESIKDPMDODGLG 180
 Qy 181 KELGEDASEVELTRNELLAYKGSSLKRLPVGMEPRILYNPLOGQKCIYQTSWSQCS 240
 Db 181 KELGEDASEVELTRNELLAYKGSSLKRLPVGMEPRILYNPLOGQKCIYQTSWSQCS 240
 Qy 241 KTCCTGISPRVNDRPECLVKERTRICETPRCGQPYSSULKKGKCSKTKSPBPVRFY 300
 Db 241 KTCCTGISPRVNDRPECLVKERTRICETPRCGQPYSSULKKGKCSKTKSPBPVRFY 300
 Qy 301 AGCLSVKRYRKPCGSCVDPGRCCCTPQLTRTVKMRFCDEGETFSKVNMDTQSCKCNYNCP 360
 Db 301 AGCLSVKRYRKPCGSCVDPGRCCCTPQLTRTVKMRFCDEGETFSKVNMDTQSCKCNYNCP 360
 Qy 361 HANEEAFFYRLENDIHKFRD 381
 Db 361 HANEEAFFYRLENDIHKFRD 381
 RESULT 2
 CYR6_MOUSE
 ID CYR6_MOUSE
 NC P18406; STANDARD; PRT; 379 AA.
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-OCT-2000 (Rel. 16, Last sequence update)
 DE CYR61 "PROTEIN PRECURSOR (3CH1)."
 GN CYR61 OR IGFBP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 RN (1) SEQUENCE FROM N.A.
 RP

STRAIN=BALB/C; TISSUE= FIBROBLAST;
 MEDLINE=92087146; PubMed=2355916;
 O'Brien T.P.; Yang G.P.; Sanders L.; Lau L.F.;
 "Expression of cyr61, a growth factor-inducible immediate-early gene.,";
 Mol. Cell. Biol. 10:3569-3577(1990).
 SEQUENCE FROM N.A.
 STRAIN=AJ; TISSUE= EMBRYONIC FIBROBLAST;
 MEDLINE=9128803; PubMed=2063642;
 Latinkic B.V.; O'Brien T.P.; Lau L.F.;
 "Promoter function and structure of the growth factor-inducible early gene cyr61.";
 Nucleic Acids Res. 19:1261-1267(1991).
 FUNCTION: MAY ACT AS ONE OF THE MANY GROWTH FACTOR-BINDING
 PROTEINS: PROMOTES PROLIFERATION, MIGRATION AND ADHESION;
 TISSUE SPECIFICITY: LOW IN KIDNEY, ADRENAL GLAND, TESTES, BRAIN,
 AND OVARY, MODERATE IN HEART, UTERUS, AND SKELETAL MUSCLE, HIGHEST
 IN LUNG.
 DEVELOPMENTAL STAGE: EXPRESSED FROM G(0)/G(1) THROUGH MID-G(1) IN
 NORMAL CELLS, AND AT A CONSTANT LEVEL IN RAPIDLY GROWING CELLS.
 INDUCTION: BY GROWTH FACTORS.
 BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE DOMAIN (CTCK).
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 DR EMBL: M32490; AA037512; 1.
 DR EMBL: X5790; CA040109; 1.
 DR PIR: A35669; A35669.
 DR MGI: 886113; CYR61.
 DR INTERPRO; IPR000359; -.
 DR INTERPRO; IPR000867; -.
 DR INTERPRO; IPR000884; -.
 DR INTERPRO; IPR01007; -.
 PFAM: PF00007; CYS_knot; 1.
 PFAM: PF00219; IGFBP; 1.
 PFAM: PF00093; wvc_1; 1.
 DR PROSITE; PS00222; IGF_BINDING; 1.
 DR PROSITE; PS01185; CYR61; 1.
 DR PROSITE; PS01225; CYR61; 1.
 DR PROSITE; PS01208; YWFC; 1.
 DR GROWTH_factor_binding; Signal; 1 24 POTENTIAL.
 FT CHAIN 25 379 CYR61 PROTEIN.
 FT DOMAIN 98 164 WFPC.
 FT DOMAIN 284 358 CTCK.
 FT DISUFLID 284 321 BY SIMILARITY.
 FT DISUFLID 301 335 BY SIMILARITY.
 FT DISUFLID 312 351 BY SIMILARITY.
 FT DISUFLID 315 353 BY SIMILARITY.
 FT DISUFLID 320 357 BY SIMILARITY.
 SQ 379 AA; 41709 MW: FA6B5014B56A8EE9 CRC64;
 Query Match Similarity 91.6%; Score 1938; DB 1; Length 379;
 Best Local Similarity 91.4%; Pred. No. 1.1e-140;
 Matches 356; Conservative 9; Mismatches 6; Gaps 2;
 Qy 1 MSSRIARALAYVTLHLTRALSTCPAACHCPLAEPKCAPAVGLYRVDGCGCKYCAKQL 60
 Db 1 MSSSTERTIAAVTLHLTRALSTCPAACHCPLAEPKCAPAVGLYRVDGCGCKYCAKQL 60
 Qy 61 NEDCSKTPQCDHTKGBCNFASTALKICRAQSGRPCYNSRIVQNGESFOPNCKHQ 120

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Db	61	NEDCSKTQPCDTIKGJUCNFGASSTALKGICRAQSEGRCPEINSRITONGESEFOPNCKHQ	1-20	FT	CHAIN	23	375	CEP-10 PROTEIN.	
QY	121	CTCIDGAVGCFPLCPQESLPLNIGCPNPRVKTGOCCEWYCDPESIKDPMEDQGLL	180	FT	DOMAIN	98	164	WIFC.	
Db	121	CTCIDGAVGCFPLCPQESLPLNIGCPNPRVKTGOCCEWYCDPESIKDPMEDQGLL	180	FT	DISULFID	281	355	CTCK.	
Db	178	KELGDASEVELTRNNEIAYKGSSKLRPLPFGMPEPRILYNPL--QGQKCVQTTSWSQ	238	FT	DISULFID	298	332	BY SIMILARITY.	
QY	181	KELGDASEVELTRNNEIAYKGSSKLRPLPFGMPEPRILYNPL--QGQKCVQTTSWSQ	238	FT	DISULFID	309	348	BY SIMILARITY.	
Db	179	--LGLDASEVELTRNNEIAYKGSSKLRPLPFGTBERVLENLPHAHGQKCVQTTSWSQ	236	FT	DISULFID	312	350	BY SIMILARITY..	
QY	239	CSKTGCGTGSTRTNDNPECRLVKPERRICEYRPCGQPVYSSLLKKRCSKTSKTKSPEPVRF	298	Query	Match	80-3%	Score 1699;	DB 1;	
Db	237	CSKSGTGSTRTNDNPECRLVKPERRICEYRPCGQPVYSSLLKKRCSKTSKTKSPEPVRF	296	Best Local Similarity	81.2%	Pred. No. 1.7-12;	Length 375;		
QY	299	TYAGGLSVKVKYRKPKVCGSCYDGRCCPTPQLTRVNRFCEDGETESKVNAMIQSCKCNYN	358	Matches	312;	Conservative	19;	Mismatches 41;	
Db	297	TYAGGLSVKVKYRKPKVCGSCYDGRCCPTPQLTRVNRFCEDGETESKVNAMIQSCKCNYN	356	Indels	12;	Gaps	7;		
QY	359	CPHANEAAFFYRLFNDIHKFRD	381	QY	1	MSSRIARALALAVVTTLHTRIAL-STCPAACHCPLDAPKCAPGVGLVLDGGCCRYCAKQ	59		
Db	357	CPHNEASFRFLYSLFNDIHKFRD	379	Db	1	MGSAGARP-ALAALICLARIALALGSPCPAVQCQCPAAAPQCAPGVGLVDPGGCCRYCAKQ	59		
RESULT	3	CE_0_CHICK	STANDARD	PRT;	375 AA.	QY	60	LNEDCSKTQCDHTKGLCLENFGASSTALKGICRAQSEGRCPEYNSRIVONGESFOPNCKH	119
		ID: P19336; AC: P19336;				Db	60	LNEDCSTRTOPCDHTKGLCLENFGASSTALKGICRAQSEGRCPEYNSRIVONGESFOPNCKH	119
						QY	120	QCTCIDGAVGCTPLCPQESLPLNIGCPNPRVKTGOCCEWYCDPESIKDPMEDQGLL	179
						Db	120	QCTCIDGAVGCTPLCPQESLPLNIGCPNPRVKTGOCCEWYCDPESIKDPMEDQGLL	179
						QY	180	GKELGFDASVEVLTRNNEIAYKGSSLLKKRPLVSEMP--RILINPLQGKCIYVTTNS	237
						Db	178	SKEFGLDASGEELTRNNEIAYKG-GLMPLPVGSEPSQRAFNP---KCIYVTTNS	232
						QY	238	QCSKRCGTCGISTRTNDNPECRLVKETRCEVRPGQPYSSLRKGKGSKTSKKSPEPYR	297
						Db	233	QCSKRCGTCGISTRTNDNPECRLVKETRCEVRPGQPYSSLRKGKGSKTSKKSPEPYR	292
						QY	298	FTYAGCLSTVKYRKPKVCGSCVDRGCTPQLTRVKTMRFCEDGETESKVNAMIQSCKCNY	357
						Db	293	FTYAGCCTVKYRKPKVCGSCVDRGCTPQLTRVKTMRFCEDGETESKVNAMIQSCKCNY	352
						QY	358	NCPHANEAAFPYRFLNDIHKFRD	381
						Db	353	NCPHANE-AFPYRFLNDIHKFRD	375
						RESULT	4	CTGF MOUSE	
						ID	CIGF_MOUSE	STANDARD;	
						AC	P22768;	PTN;	348 AA.
						DT	01-DEC-1992	(Rel. 24, Created)	
						DT	01-DEC-1992	(Rel. 24, Last sequence update)	
						DT	15-JUL-1998	(Rel. 36, Last annotation update)	
						DE	CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (CTGF) (FISP-12 PROTEIN).		
						GN	CTGF OR FISP12 OR FISP-12.		
						OS	Mus musculus (Mouse).		
						OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.		
						RN	[1]		
						RN		SEQUENCE FROM N.A.	
						RX		MEDLINE=91163290; PubMed=1888688;	
						RX		Medline=91163290; PubMed=1888688;	
						RA		Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RA		Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
						RT		RT identification of a gene family regulated by transforming growth factor-beta.;	
						RT		RT structure, mapping, and expression of fisp-12, a growth factor-	
						RL		RL cell growth differ. 2:225-233(1991).	
						RL		RL sequence from N.A.	
						RP		RP Medline=91163290; PubMed=1888688;	
						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
						RP		RP RT identification of a gene family regulated by transforming growth factor-beta.;	
						RP		RP RT structure, mapping, and expression of fisp-12, a growth factor-	
						RP		RP RL cell growth differ. 2:225-233(1991).	
						RP		RP sequence from N.A.	
						RP		RP Medline=91163290; PubMed=1888688;	
						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
						RP		RP RT identification of a gene family regulated by transforming growth factor-beta.;	
						RP		RP RT structure, mapping, and expression of fisp-12, a growth factor-	
						RP		RP RL cell growth differ. 2:225-233(1991).	
						RP		RP sequence from N.A.	
						RP		RP Medline=91163290; PubMed=1888688;	
						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
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						RP		RP RL cell growth differ. 2:225-233(1991).	
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						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
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						RP		RP RL cell growth differ. 2:225-233(1991).	
						RP		RP sequence from N.A.	
						RP		RP Medline=91163290; PubMed=1888688;	
						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
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						RP		RP sequence from N.A.	
						RP		RP Medline=91163290; PubMed=1888688;	
						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
						RP		RP RT identification of a gene family regulated by transforming growth factor-beta.;	
						RP		RP RT structure, mapping, and expression of fisp-12, a growth factor-	
						RP		RP RL cell growth differ. 2:225-233(1991).	
						RP		RP sequence from N.A.	
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						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
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						RP		RP RL cell growth differ. 2:225-233(1991).	
						RP		RP sequence from N.A.	
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						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
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						RP		RP sequence from N.A.	
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						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
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						RP		RP RT structure, mapping, and expression of fisp-12, a growth factor-	
						RP		RP RL cell growth differ. 2:225-233(1991).	
						RP		RP sequence from N.A.	
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						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
						RP		RP RT identification of a gene family regulated by transforming growth factor-beta.;	
						RP		RP RT structure, mapping, and expression of fisp-12, a growth factor-	
						RP		RP RL cell growth differ. 2:225-233(1991).	
						RP		RP sequence from N.A.	
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						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
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						RP		RP sequence from N.A.	
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						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
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						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
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						RP		RP sequence from N.A.	
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						RP		RP Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;	
						RP		RP Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;	
						RP		RP RT identification of a gene family regulated by transforming growth factor-beta.;	
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						RP		RP RT identification of a gene family regulated by transforming growth factor-beta.;	
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						RP		RP RL cell growth differ. 2:225-233(1991).	
						RP		RP sequence from N.A.	
						RP		RP Medline=91163290; PubMed=1888688;	
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